

Fig. 1

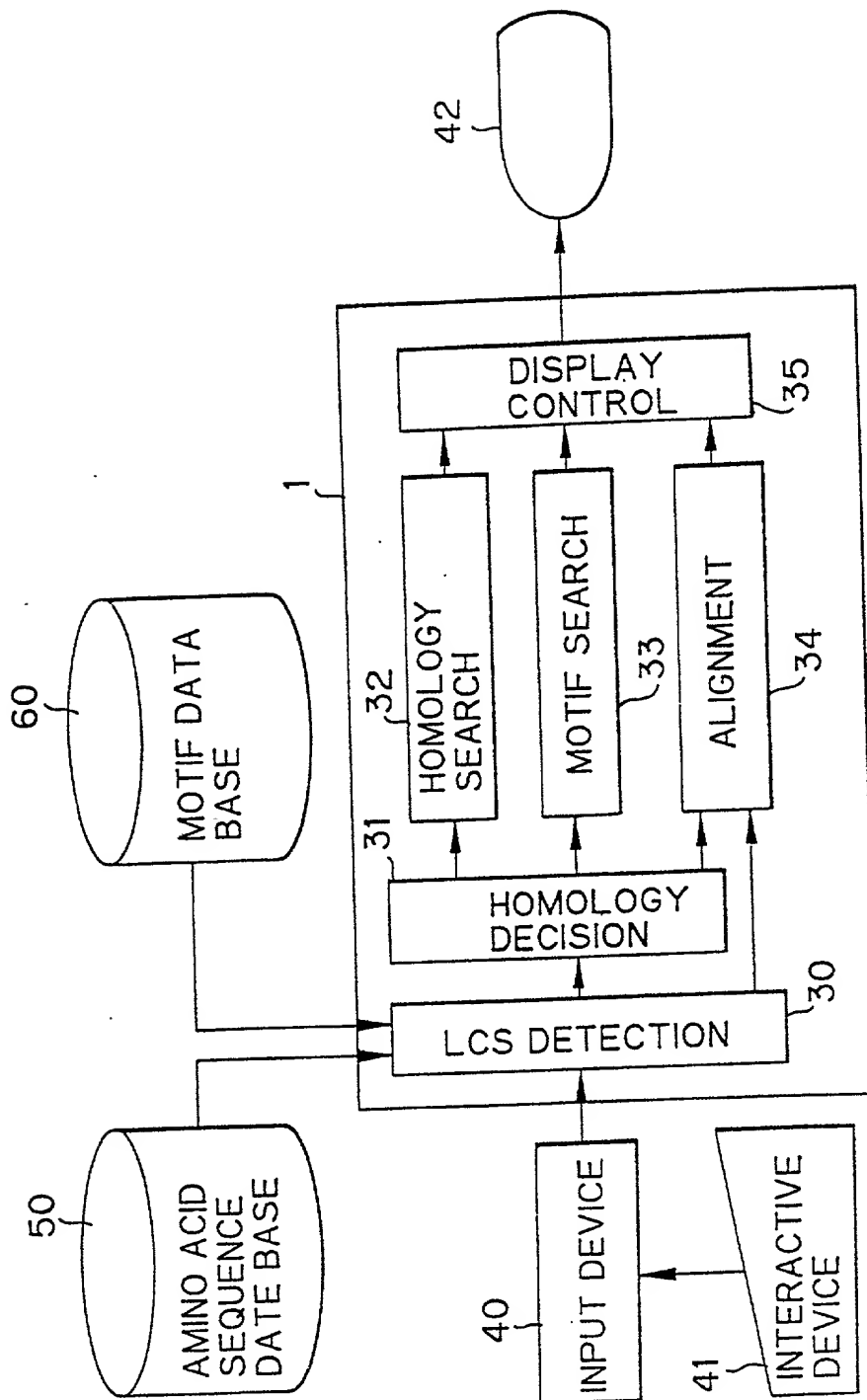


Fig. 2

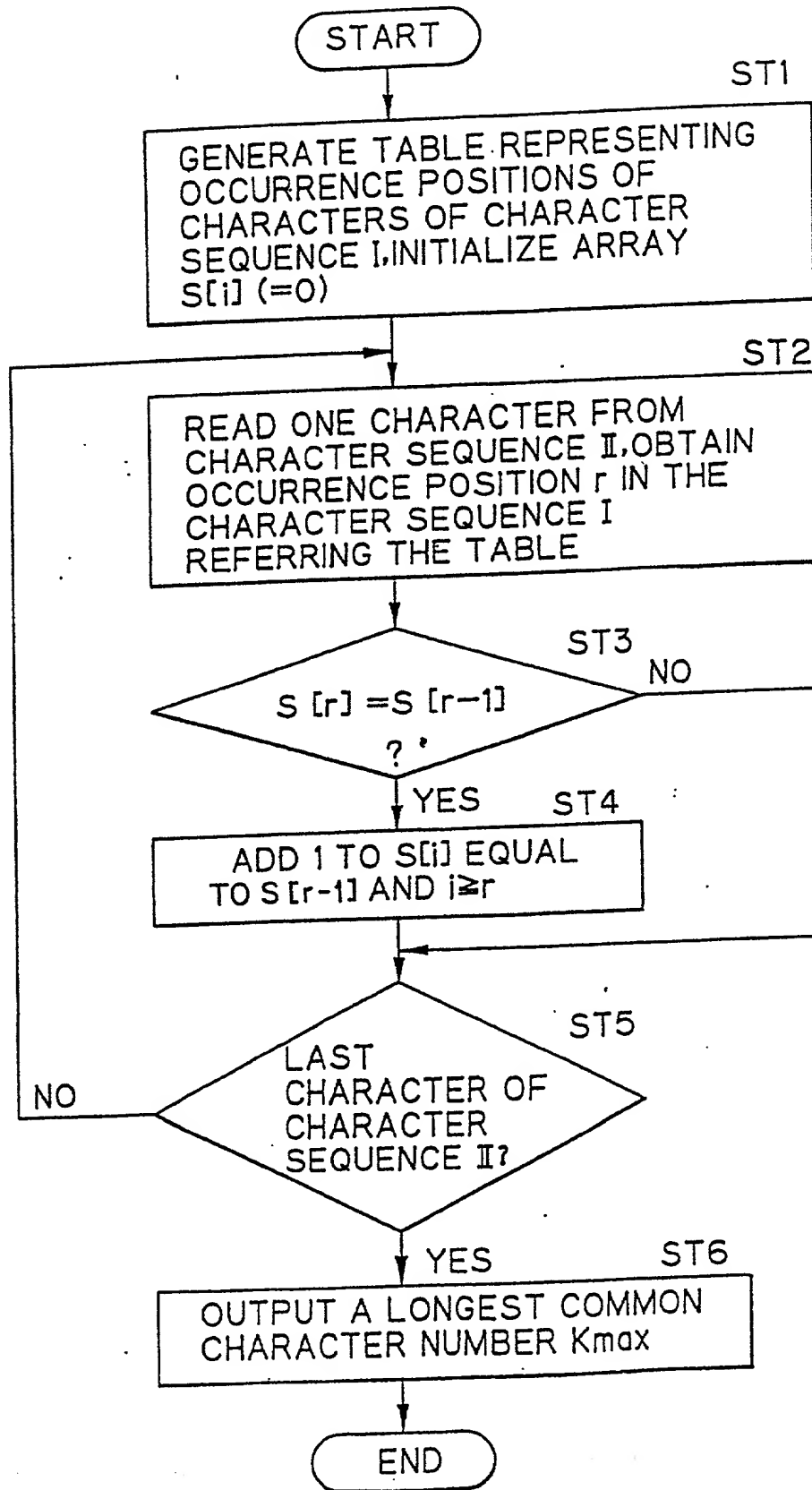


Fig. 3

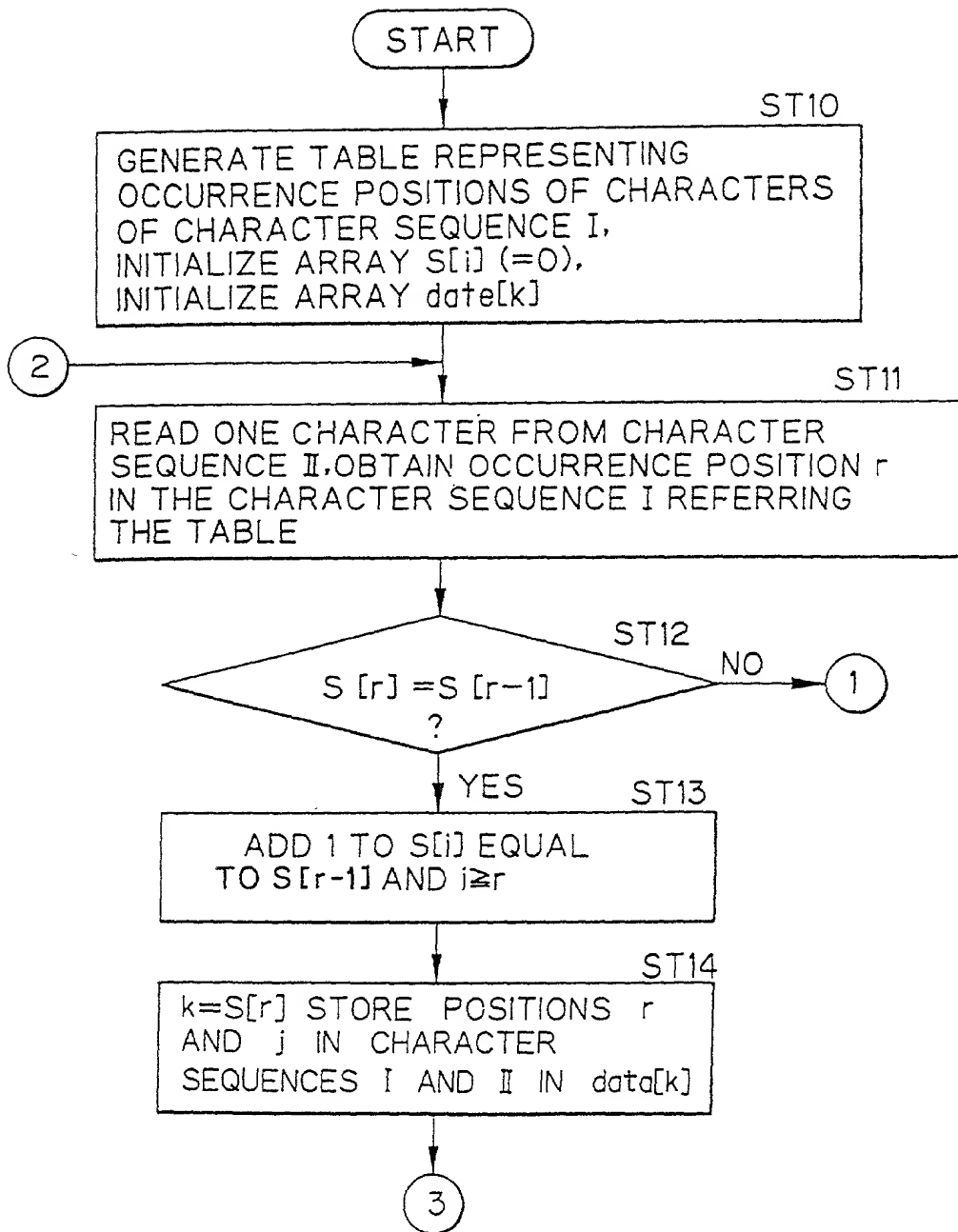
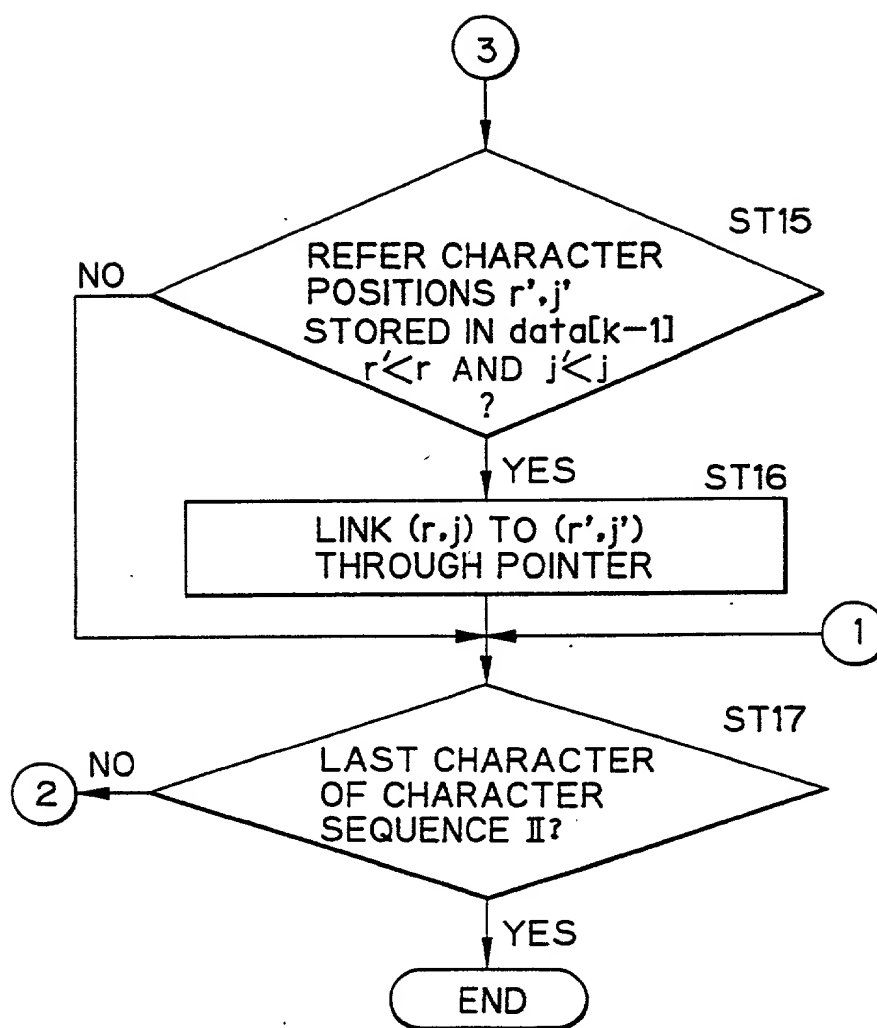


Fig. 4



*Fig. 5*

CHARACTER SEQUENCE I="ABCBDAB"

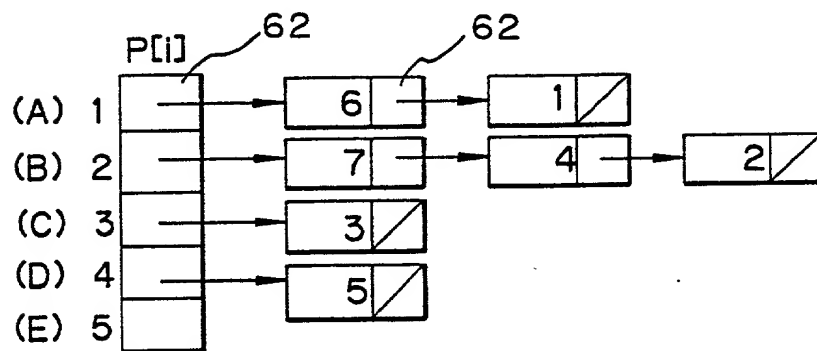






Fig. 8

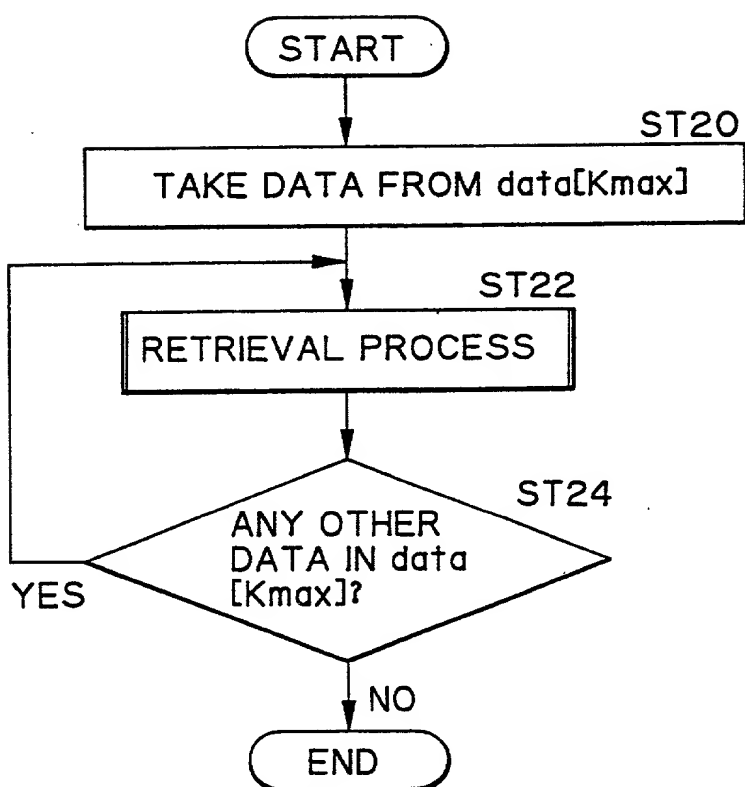
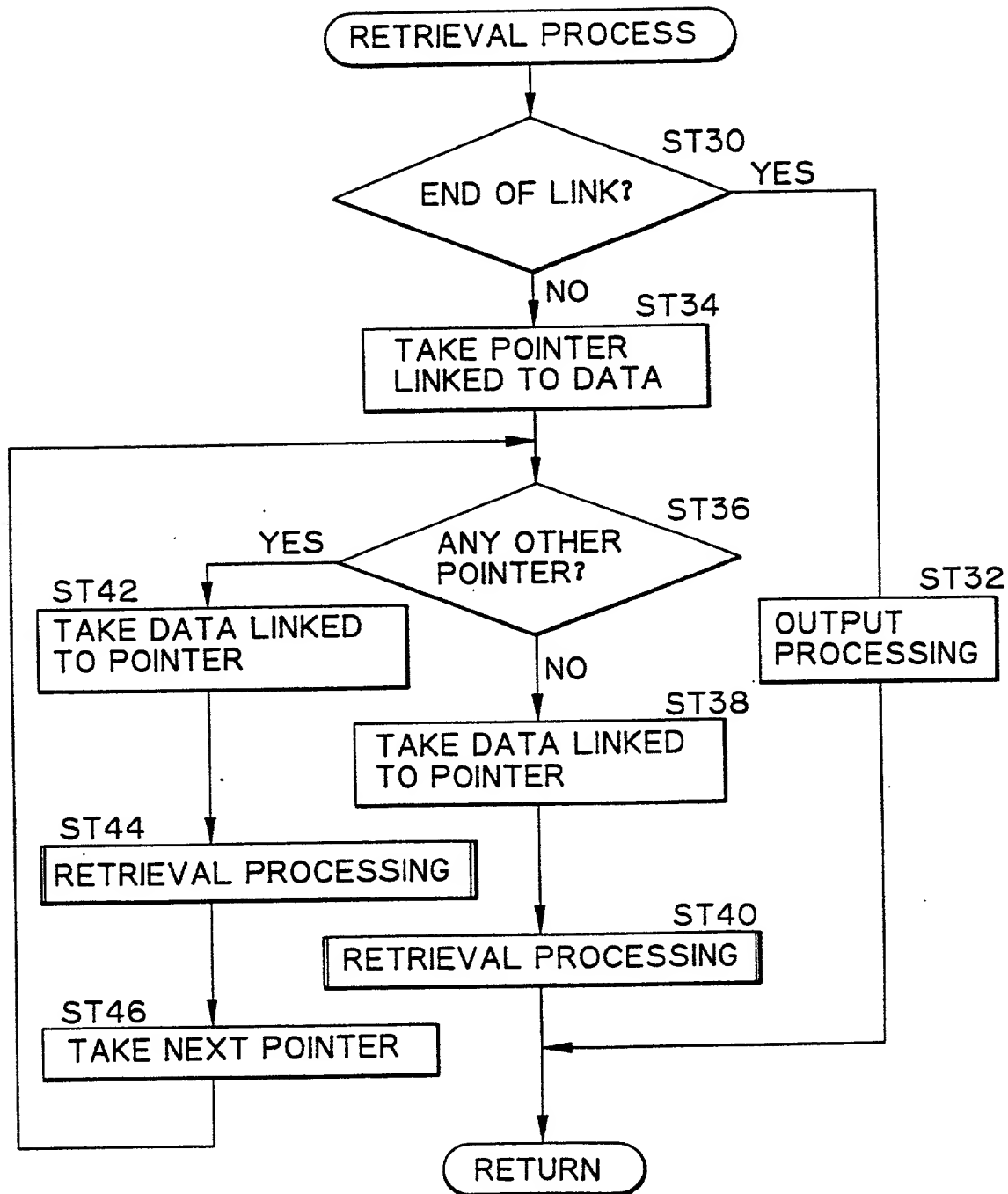




Fig. 9



**Fig. 10**

human : GDVEKGKKIFIMKCSQCHTVEGGKHKTGPNLHGLFGRK  
bacterium : EGDAAAGEKVSCKCLACHTFDQGGANKVGPNNLFGVF

LCS : GD{x3.3}G{x0.1}K{x0.2}K{x4.0}KC{x2.2}CHT{x3.3}GG{x2.2}K  
GD{x1.4}E{x0.2}K{x0.2}K{x0.4}KC{x2.2}CHT{x3.3}GG{x2.2}K

homology : 47%

*Fig. 11*

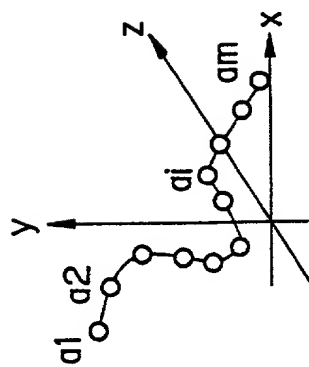
Rat : MSLAILRVIRLVRVFRIFKLSRHSKGLQILGRTLKASMRELGLLFFIGVV

leucinzip. L(6)L(6)L(6)L(6)L

*Fig. 12*

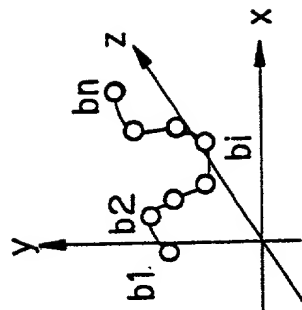
human : GDVEK G K KIFIMKCSQCHTVEKGG KHKTGPNLHGLFGRK ...  
bacterium : E GDAAAGEKVS KCLACHTFDQGGANKV GPNPN LFGVF...

Fig. 13 A



$A = \{a_1, a_2, \dots, a_i, \dots, a_m\}$

Fig. 13 B



$B = \{b_1, b_2, \dots, b_i, \dots, b_n\}$

Fig. 13 C

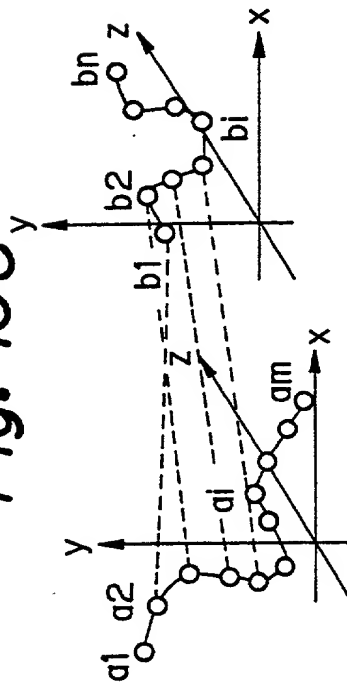


Fig. 13 D

$$r.m.s.d = \frac{\sqrt{\sum_{k=1}^n w_k (U_{b_k} - a_k)^2}}{n}$$

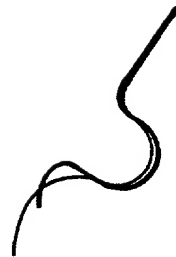
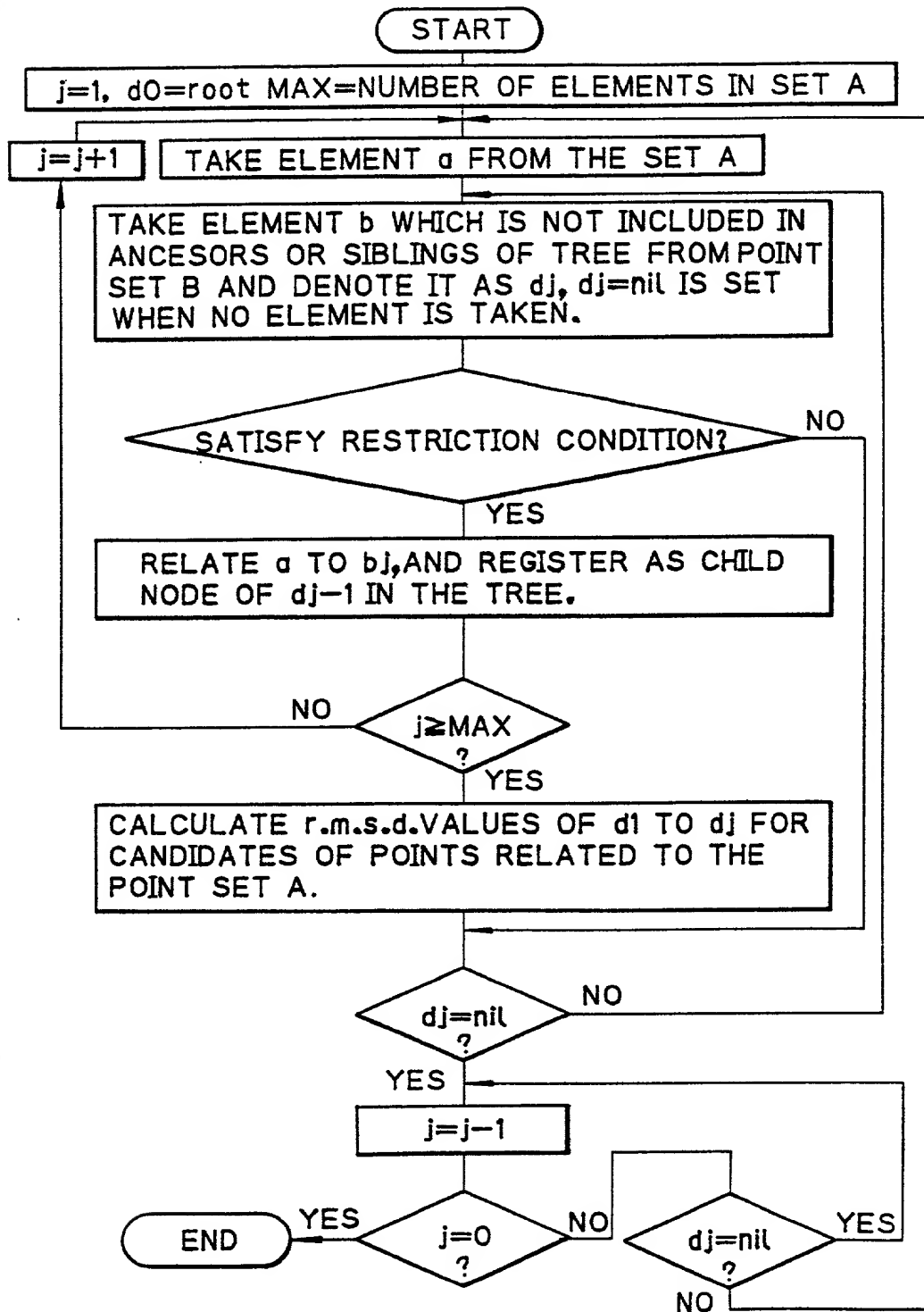


Fig. 15



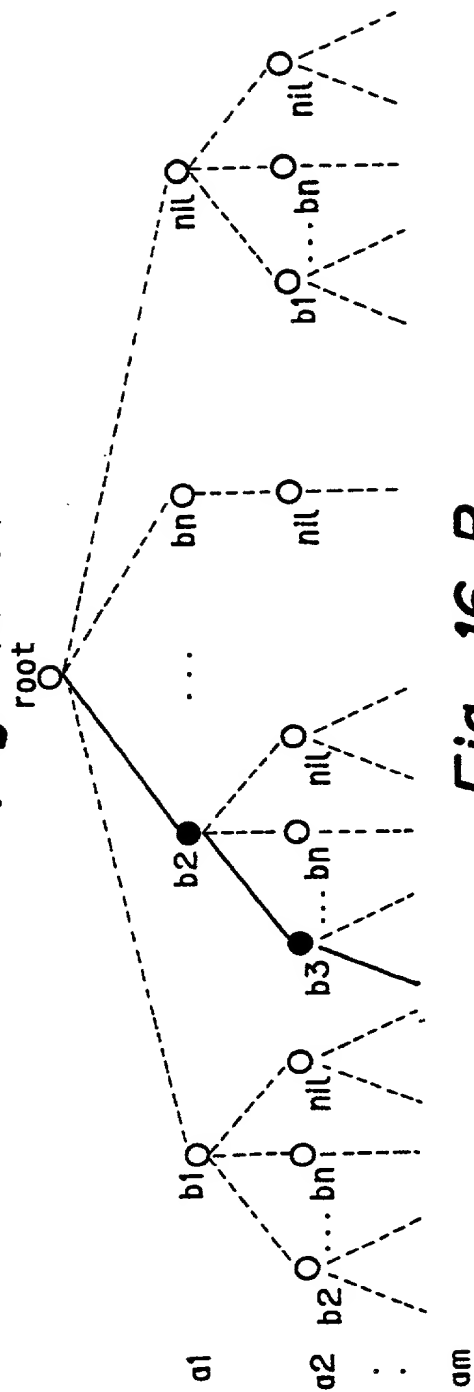
root



root



**Fig. 16 A**



**Fig. 16 B**

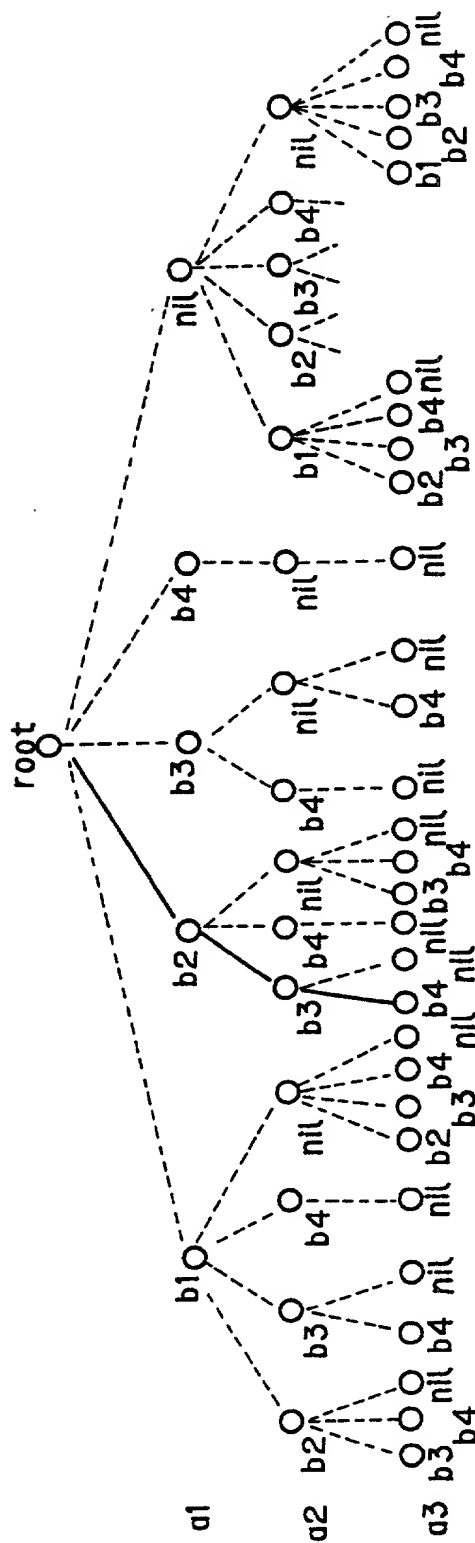




Fig. 17

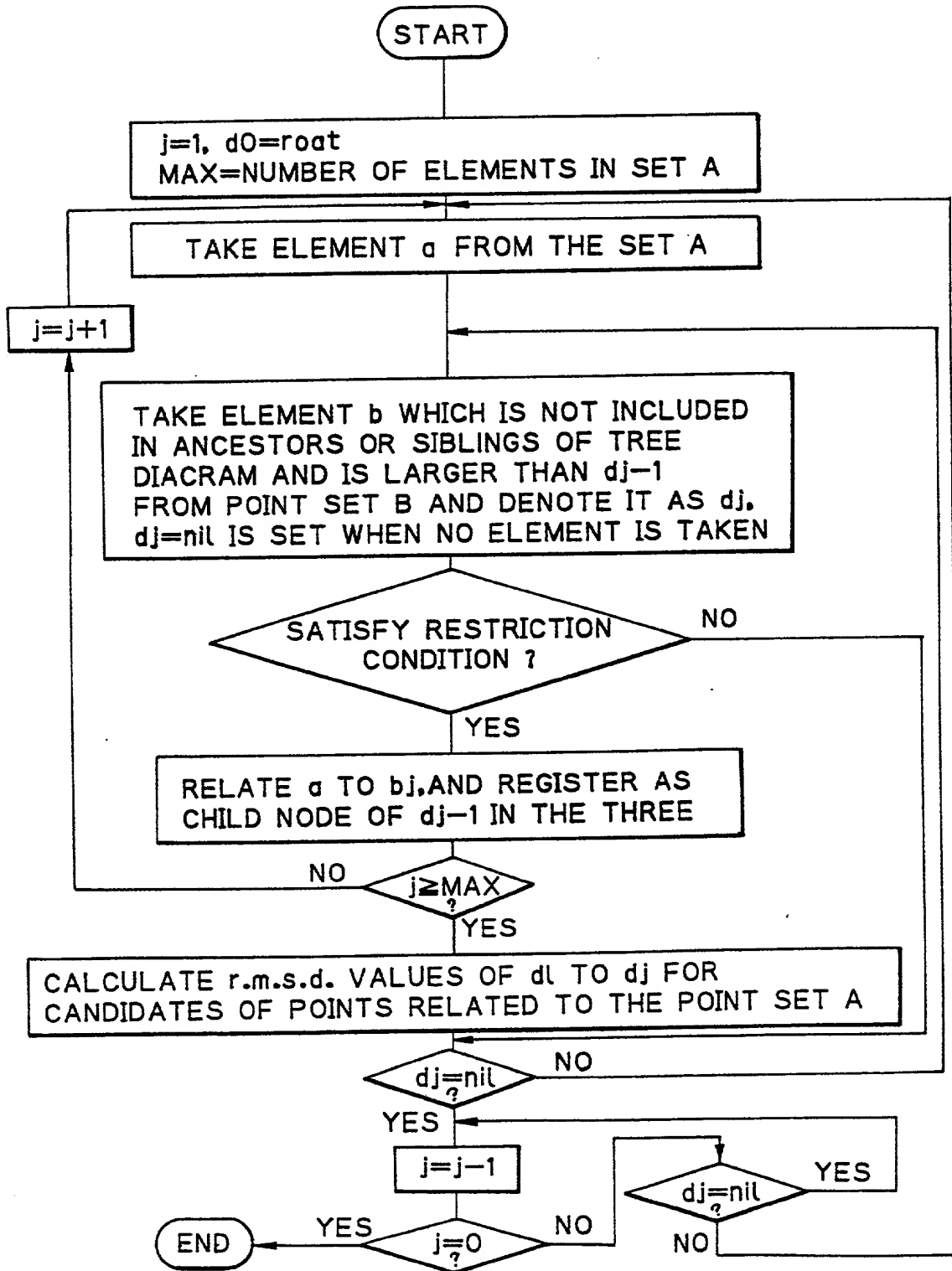




Fig. 19 A

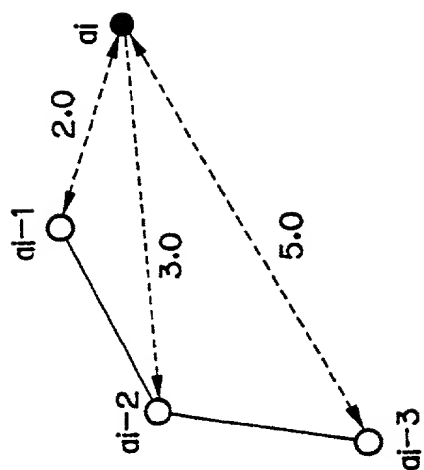


Fig. 19 B

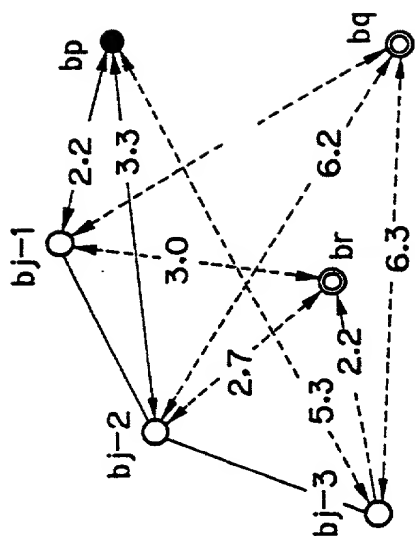


Fig. 20 A

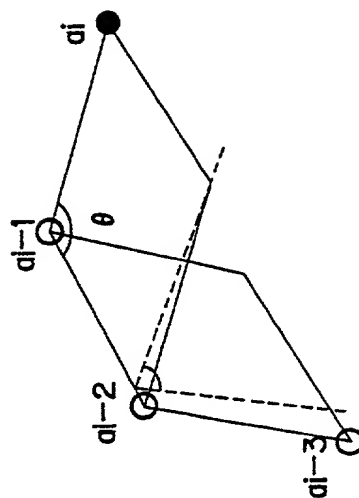


Fig. 20 B

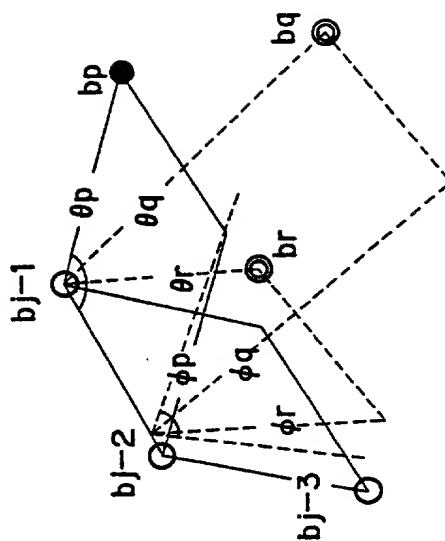


Fig. 21

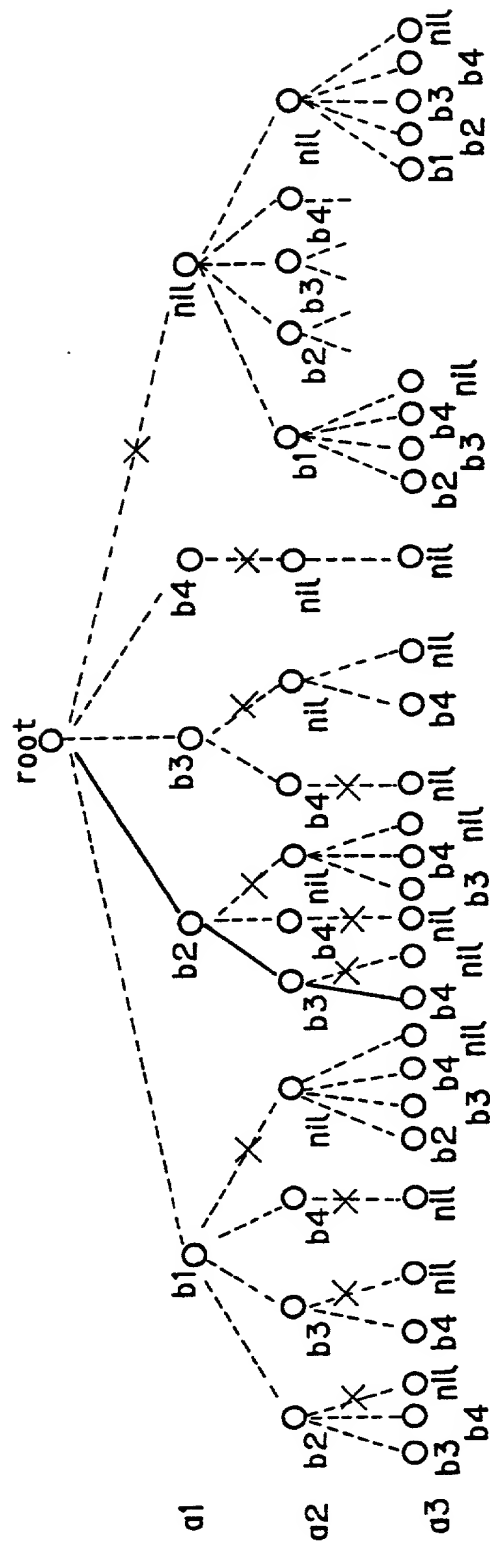
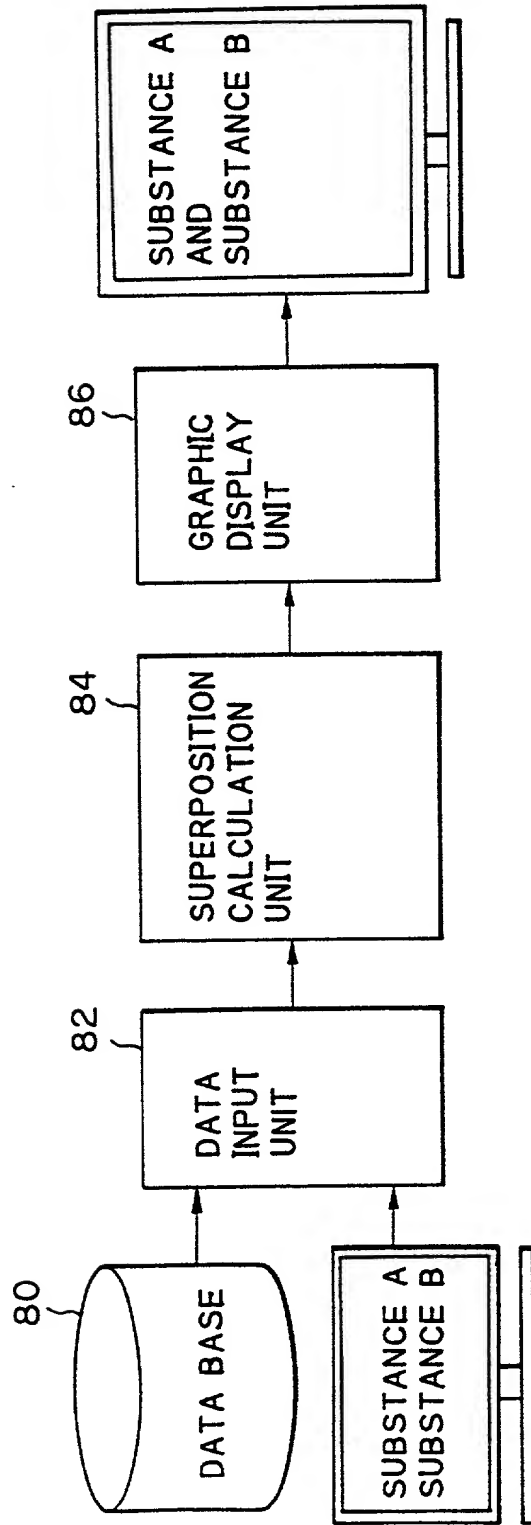


Fig. 22



**Fig. 23 A**

1	TEEQIAEFKE	AFSLFDKDG
21	GTITTKELGT	VMRSLGQNPT
41	EAELQDMINE	VDADGNGTID
61	FPEFLTMMAR	KMKD TDSEEE
81	IREAFRVFDK	DGNGYISAAE
101	LRHVMTNLGE	KLTD EEVDEM
121	IREANIDGDG	QVNYEEFVQM
141	MTA	

AMINO ACID SEQUENCE OF CALMODULIN  
(EXCERPT FROM PDB)

**Fig. 23 B**

1	AMDQQAEARA	FLSEEMIAEF
21	KAAFD MF DAD	GGGDI STKEL
41	GTVMRMLGQN	PTKEELDAII
61	EEVDE DGS GT	IDFEEFLVM
81	VRQMKEDAKG	KSEEEELADCF
101	RIFDKNADGF	IDIEELGEIL
121	RATGEHVTEE	DIEDLMKDSD
141	KNNDGRIDFD	EFLKMMEGVQ
161		

AMINO ACID SEQUENCE OF TROPONIN C  
(EXCERPT FROM PDB)

Fig. 24 A

CALMODULIN

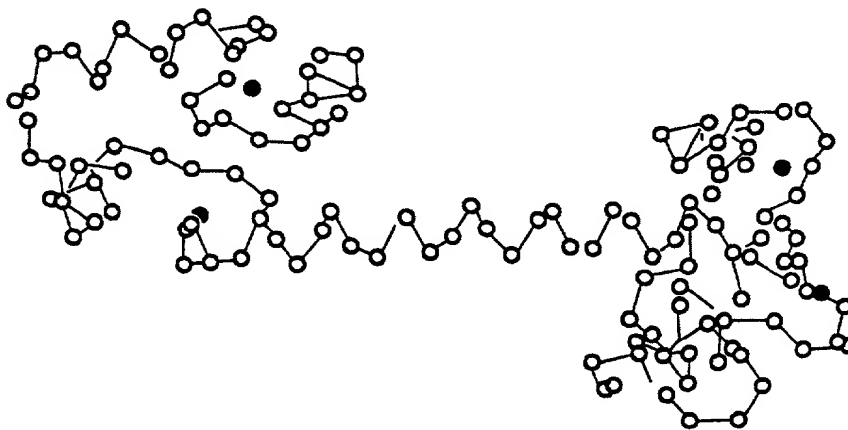


Fig. 24 B

TROPONIN C

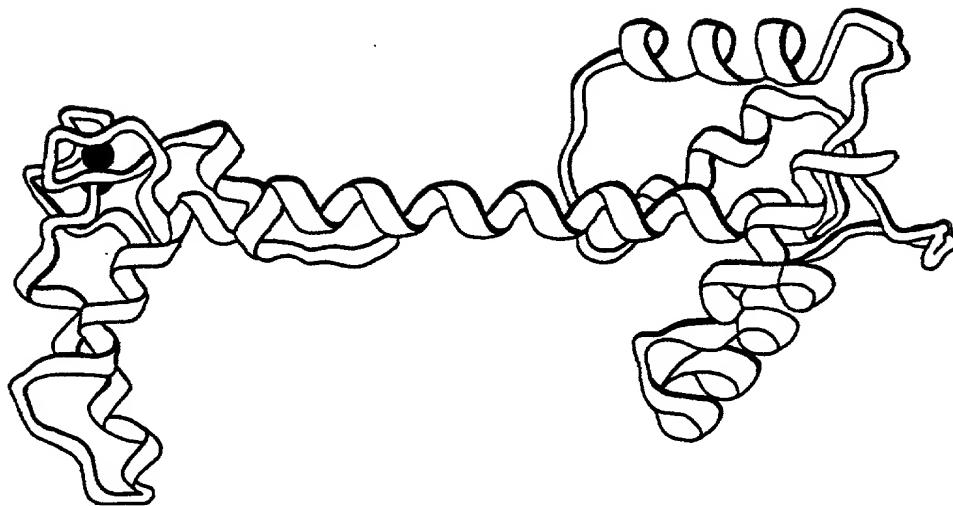






Fig. 26

96	L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	< target	>
97	I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe	>
98	111	112	113	114	115	116	117	118	119	120	121	122	123				
99	I	D	I	E	E	L	G	E	I	L	R	A	T		< target	>	
100	I	S	A	A	E	L	R	H	V	M	T	N	L		< probe	>	
101	132	133	134	135	136	137	138	139	140	141	142	143	144	145			
102	I	E	D	L	M	K	D	S	D	K	N	N	D	G	< target	>	
103	V	D	E	M	I	R	E	A	N	I	D	G	D	G	< probe	>	
104	146	147	148	149	150	151	152	153	154	155	156	157	158				
105	R	I	D	F	D	E	F	L	K	M	M	E	G		< target	>	
106	Q	V	N	Y	E	E	F	V	Q	M	M	T	A		< probe	>	

$$\text{rmsd} = 0.823665$$

Fig. 27

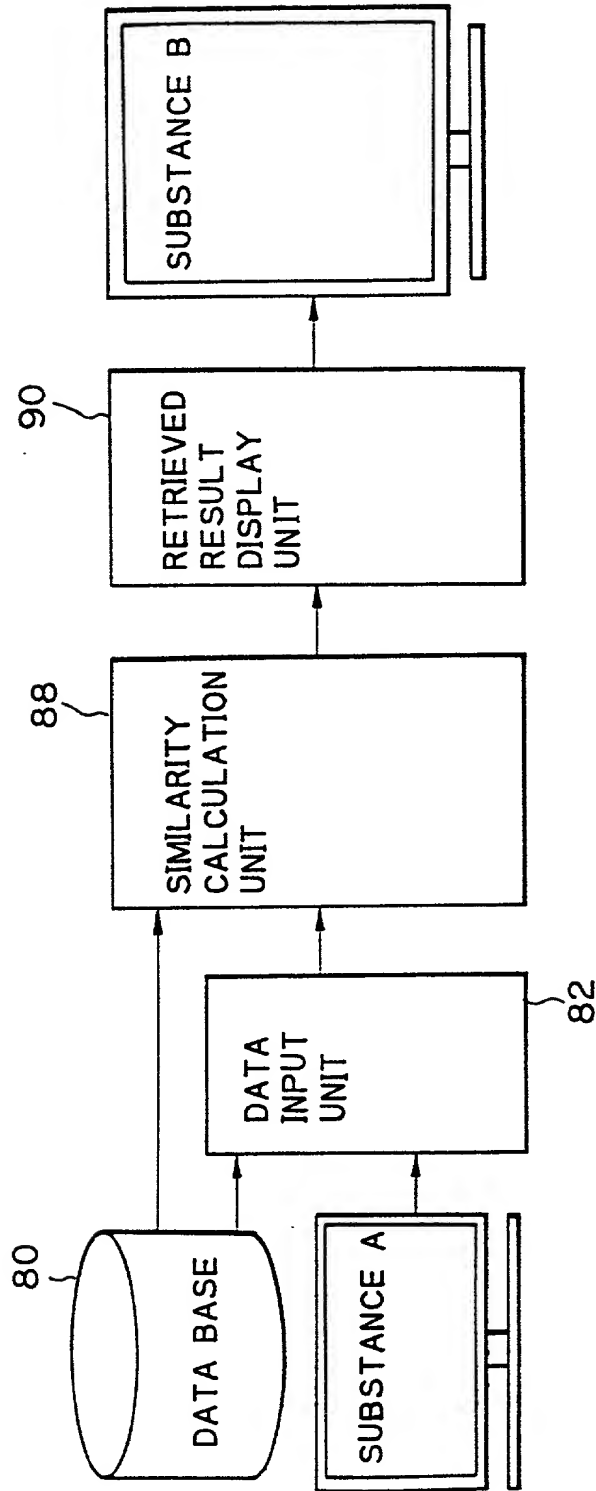


Fig. 28

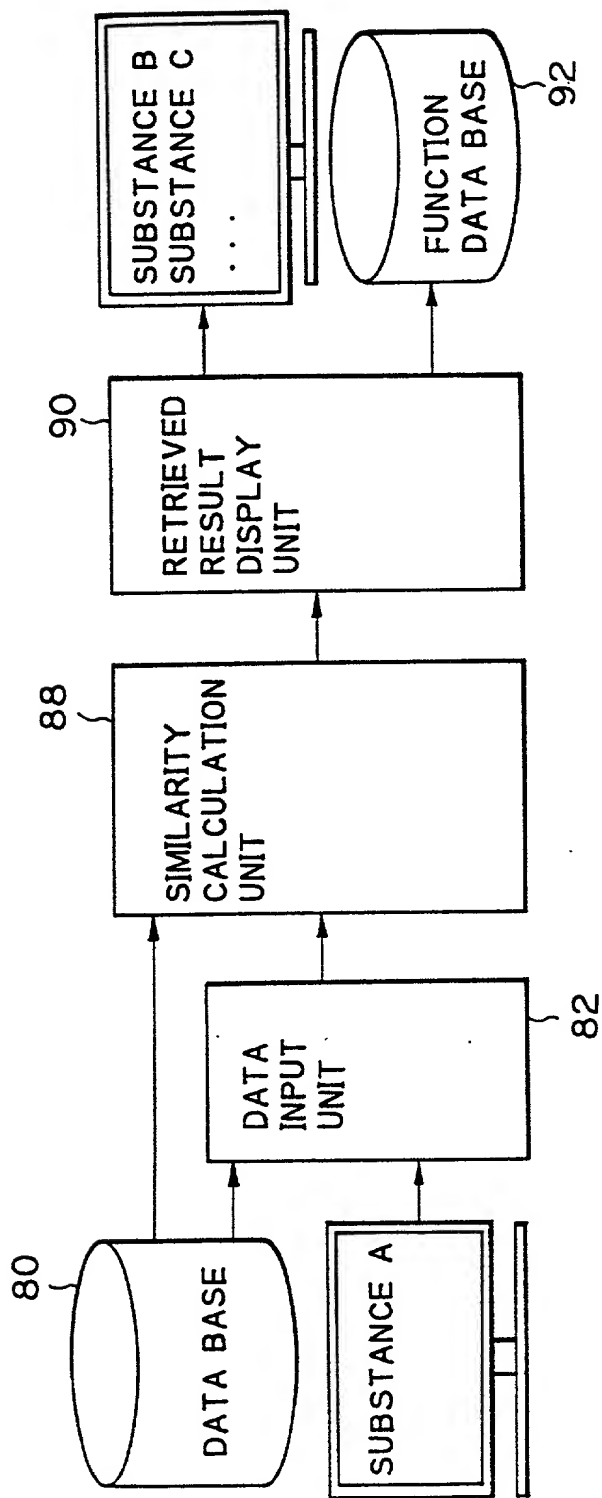




Fig. 30

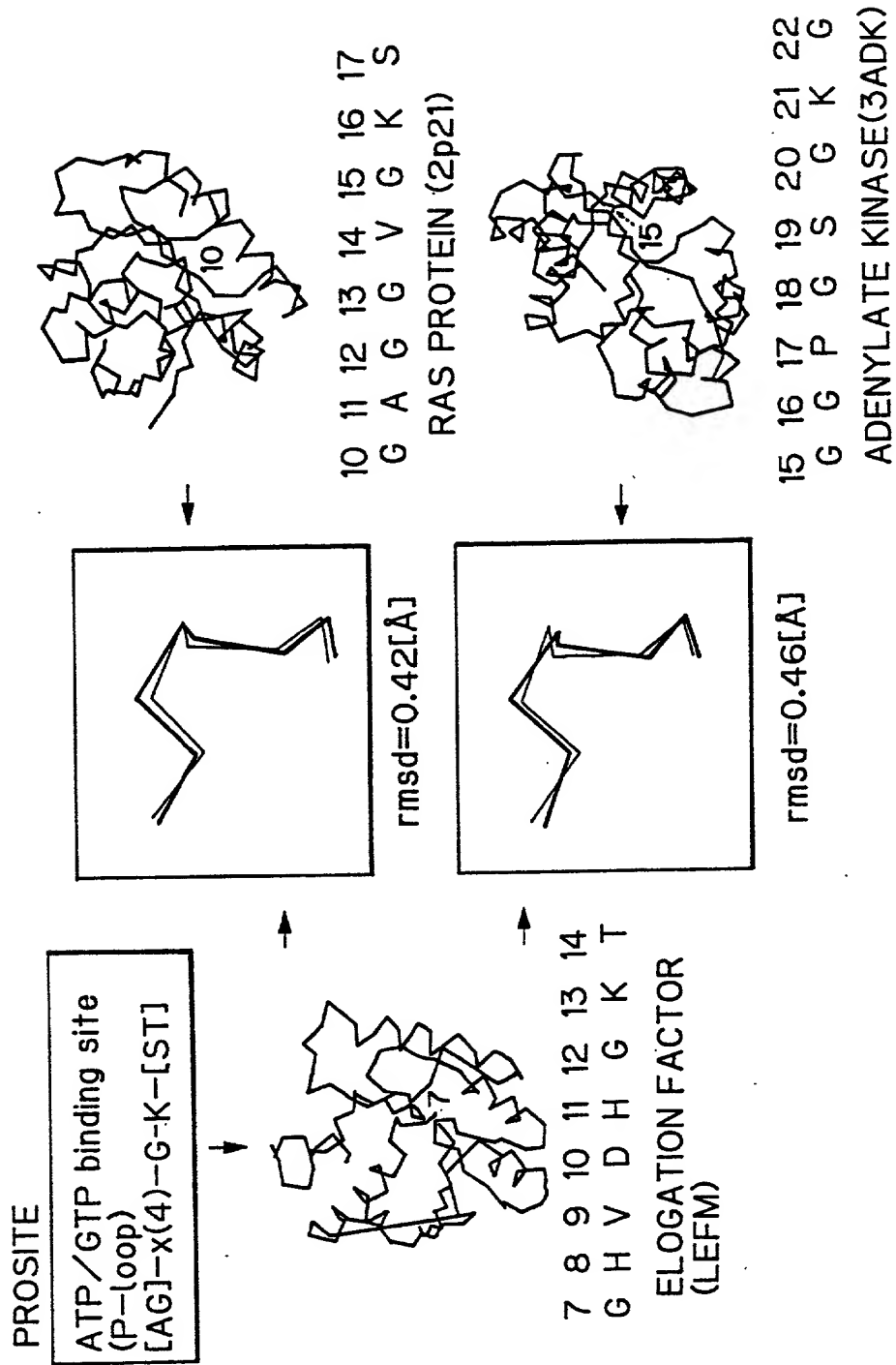


Fig. 31

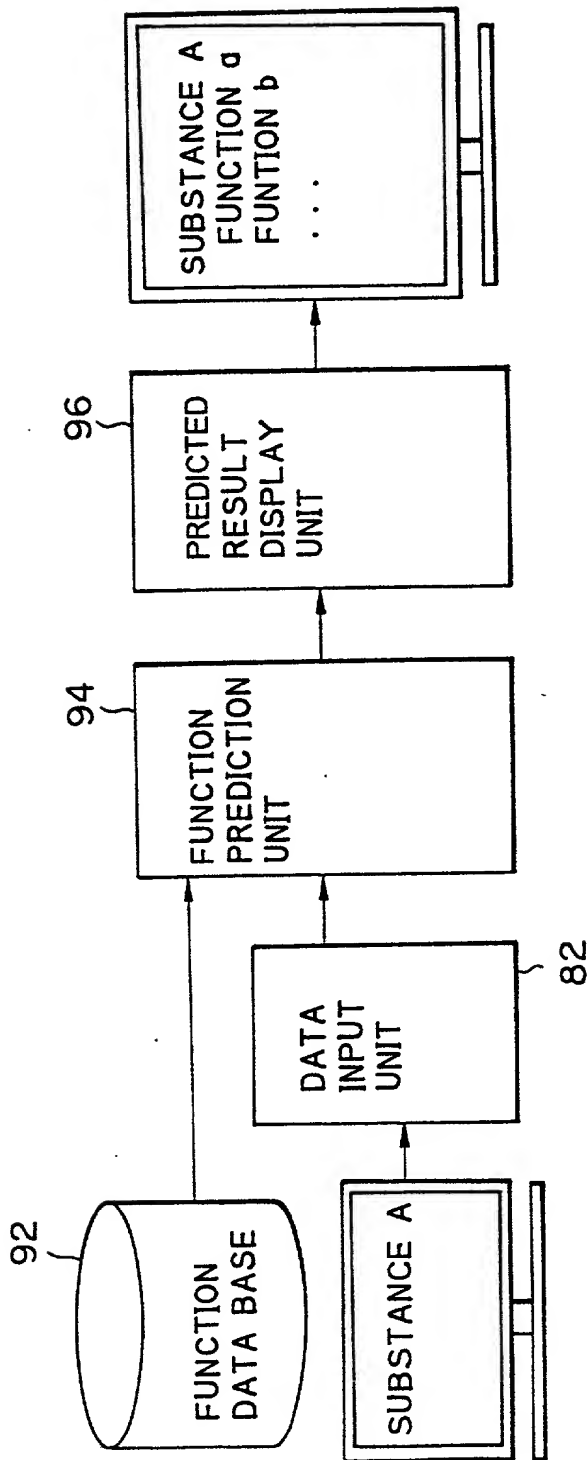


Fig. 32 A

Fig. 32 B

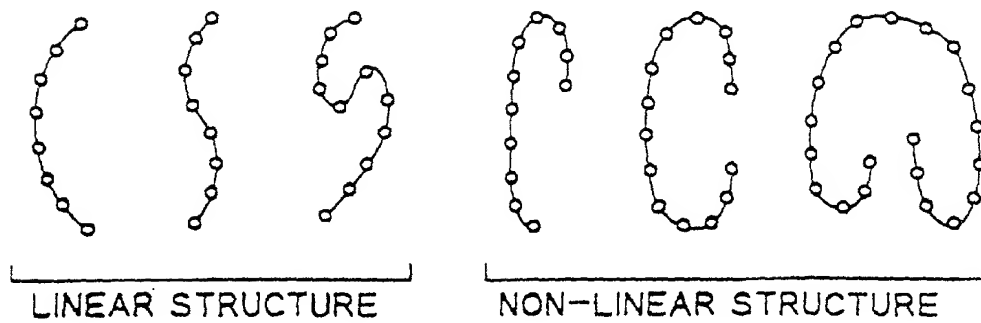
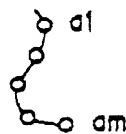
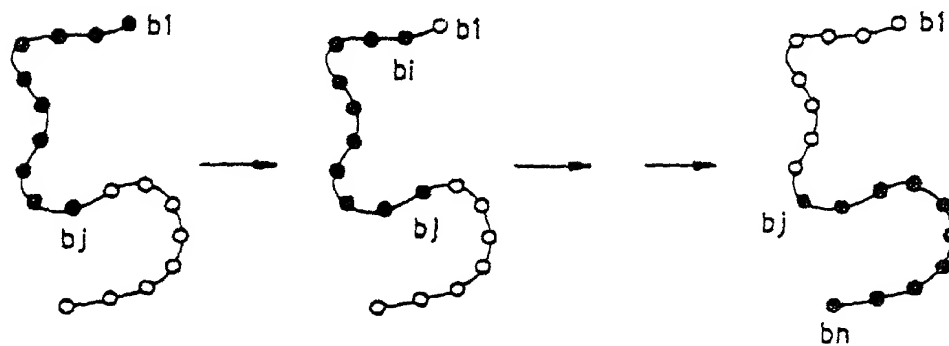


Fig. 33

WHEN  $f(x)=2x$



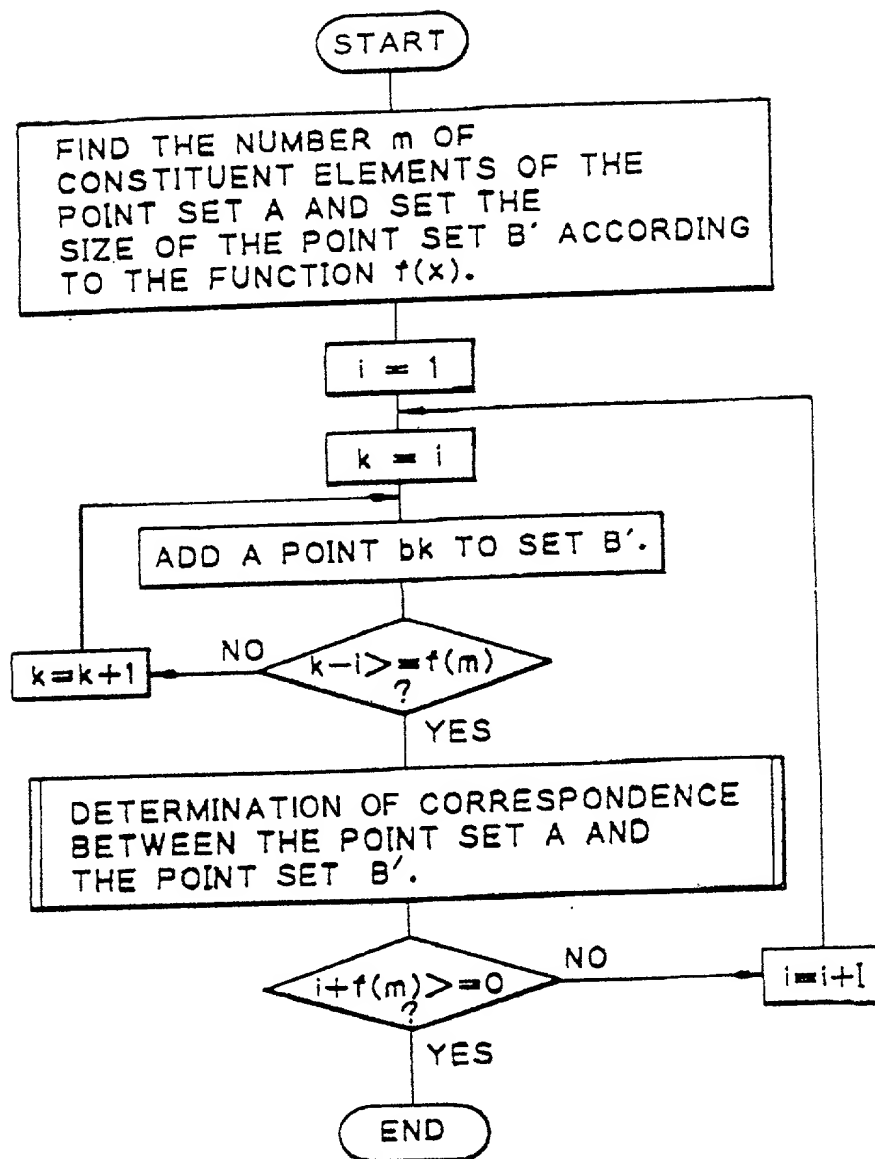
$A=\{a_1, \dots, a_m\}$



$B=\{b_1, \dots, b_i, \dots, b_j, \dots, b_n\}$

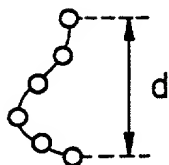
FIG. 32 A

Fig. 34



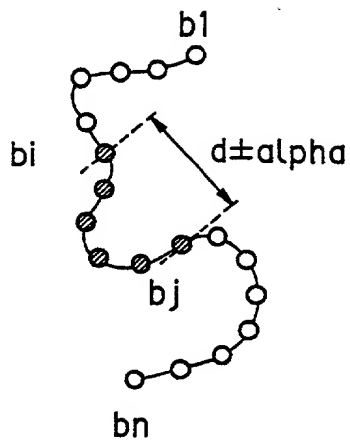


*Fig. 35 A*



$$A = \{a_1, a_2, \dots, a_m\}$$

*Fig. 35 B*



$$B = \{b_1, \dots, b_i, \dots, b_j, \dots, b_n\}$$

Fig. 36

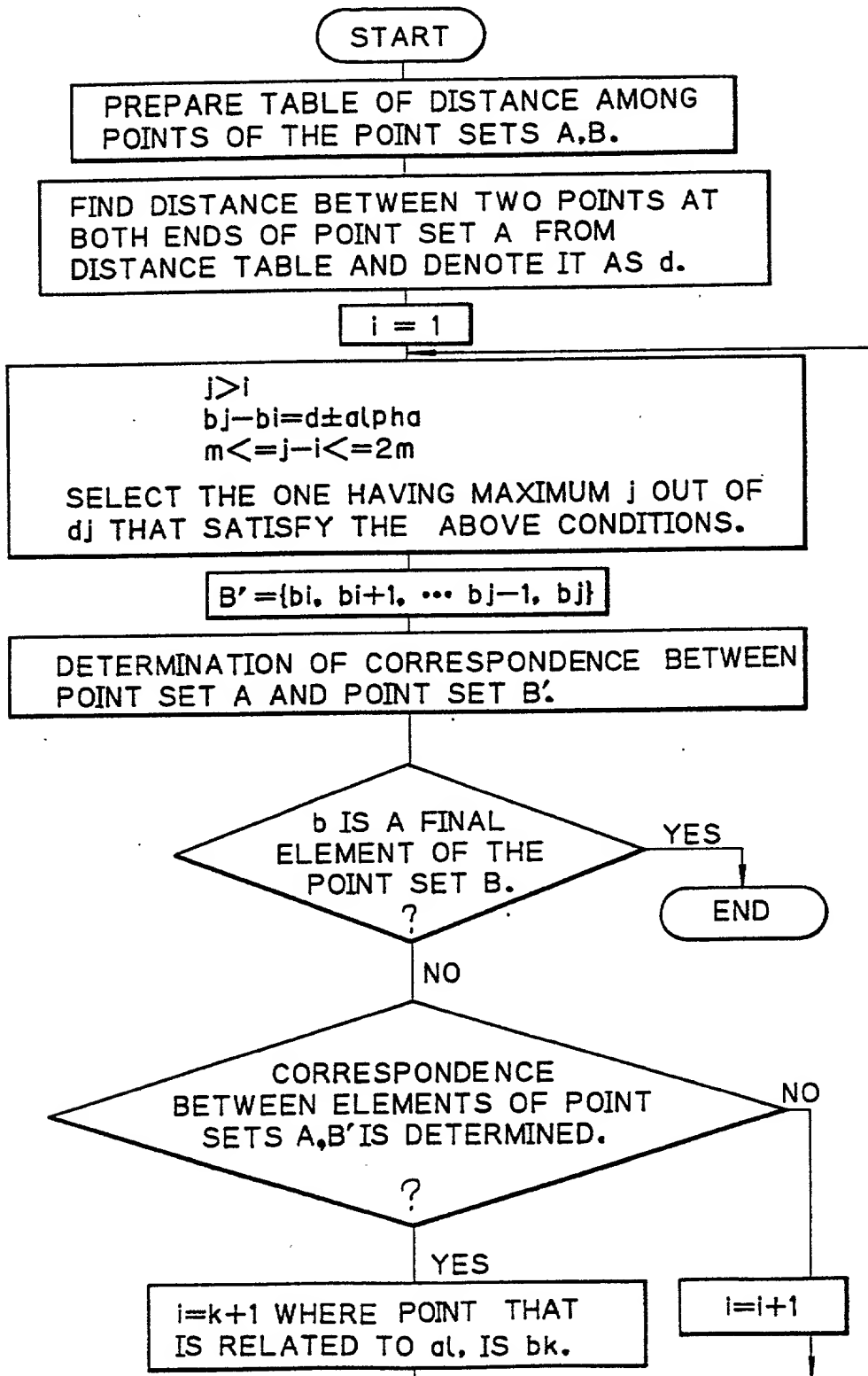
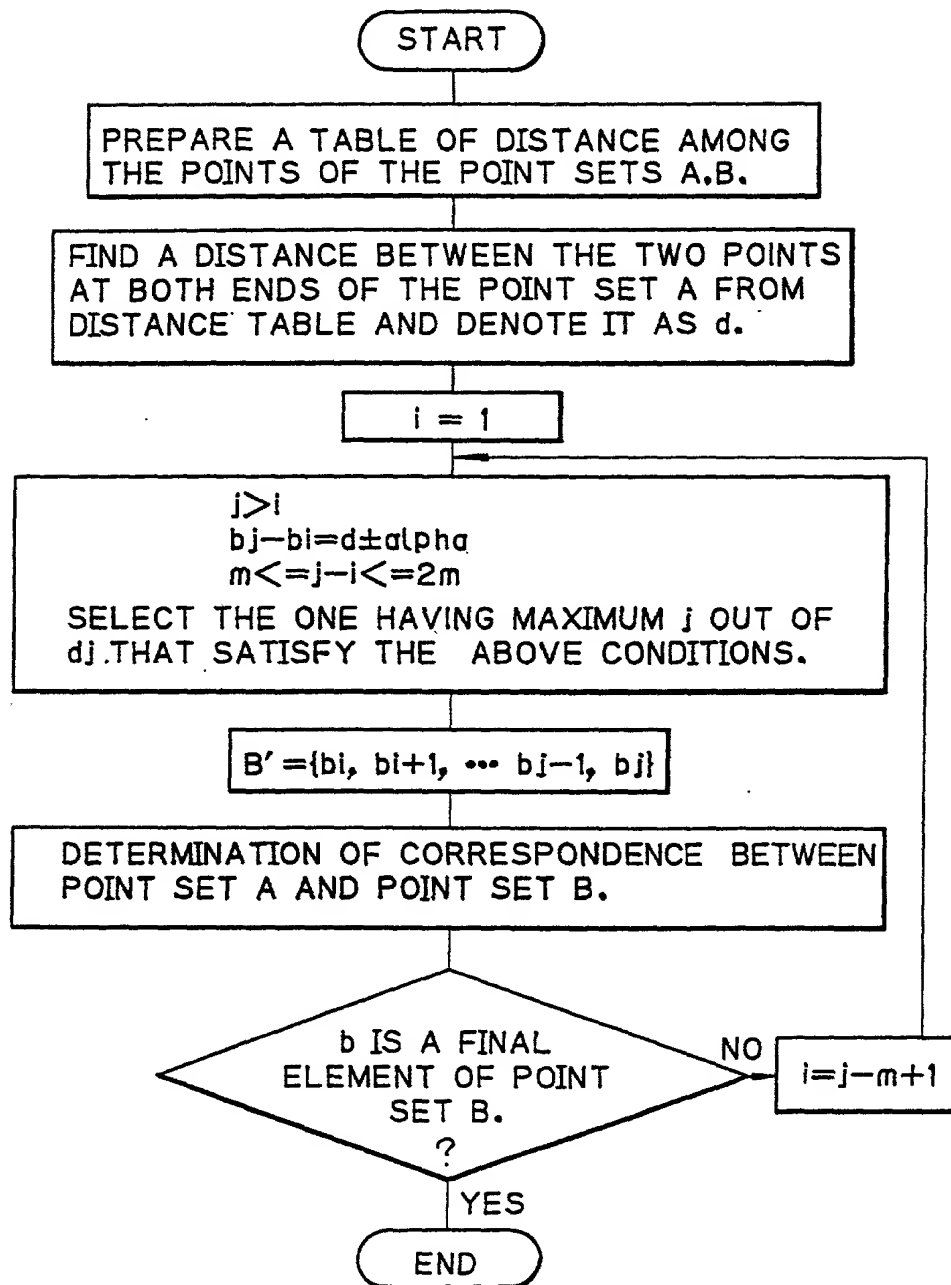


Fig. 37



T0220 60860660

**Fig. 38 A**

1	I	V	G	G	Y	T	C	C	A	N	T	V	P	Y	Q	V	S	L	N	S
21	G	Y	H	F	C	G	G	S	L	I	N	S	Q	W	V	V	S	A	A	H
41	C	Y	K	S	G	I	Q	V	R	L	G	E	D	N	I	N	V	V	E	G
61	N	E	Q	F	I	S	A	S	K	S	I	V	H	P	S	Y	N	S	N	T
81	L	N	N	D	I	M	L	I	K	L	K	S	A	A	S	L	N	S	R	V
101	A	S	I	S	L	P	T	S	C	A	S	A	G	T	Q	C	L	I	S	G
121	W	G	N	T	K	S	S	G	T	S	Y	P	D	V	L	K	C	L	K	A
141	P	I	L	S	D	S	S	C	K	S	A	Y	P	G	Q	I	T	S	N	M
161	F	C	A	G	Y	L	E	G	G	K	D	S	C	Q	G	D	S	G	G	P
181	V	V	C	S	G	K	L	Q	G	I	V	S	W	G	S	G	C	A	Q	K
201	N	K	P	G	V	Y	T	K	V	C	N	Y	V	S	W	I	K	Q	T	I
221	A	S	N																	

AMINO ACID SEQUENCE OF TRYPSIN (EXCERPT FROM PDB)

**Fig. 38 B**

1	V	V	G	G	T	E	A	Q	R	N	S	W	P	S	Q	I	S	L	Q	Y
21	R	S	G	S	S	W	A	H	T	C	G	G	T	L	I	R	Q	N	W	V
41	M	T	A	A	H	C	V	D	R	E	L	T	F	R	V	V	V	G	E	H
61	N	L	N	Q	N	N	G	T	E	Q	Y	V	G	V	Q	K	I	V	V	
81	P	Y	W	N	T	D	D	V	A	A	G	Y	D	I	A	L	L	R	L	A
101	Q	S	V	T	L	N	S	Y	V	Q	L	G	V	L	P	R	A	G	T	I
121	L	A	N	S	P	C	Y	I	T	T	G	W	G	L	T	R	T	N	G	Q
141	L	A	Q	T	L	Q	Q	A	Y	L	P	T	V	D	Y	A	I	C	S	S
161	S	S	Y	W	G	S	T	V	K	N	S	M	V	C	A	G	G	D	G	V
181	R	S	G	C	Q	G	D	S	G	G	P	L	H	C	L	V	N	G	Q	Y
201	A	V	H	G	V	T	S	F	V	S	R	L	G	C	N	V	T	R	K	P
221	T	V	F	T	R	V	S	A	Y	I	S	W	I	N	N	V	I	A	S	N

AMINO ACID SEQUENCE OF ELASTASE (EXCERPT FROM PDB)

**Fig. 39 A**

Key site number 36 – 41 in Trypsin

41	42	43	44	45	46		
M	T	A	A	H	C	< target >	
V	S	A	A	H	C	< probe >	

d = 12.070038 [A]

r.m.s.d. = 0.061077 [A]

The number of atoms in a probe = 6

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF HISTIDINE ACTIVE SITES

**Fig. 39 B**

Key site number 175 – 179 in Trypsin

186	187	188	189	190		
G	D	S	G	G	< target >	
G	D	S	G	G	< probe >	

d = 8.922721 [A]

r.m.s.d. = 0.092879 [A]

The number of atoms in a probe = 5

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF SERINE ACTIVE SITES

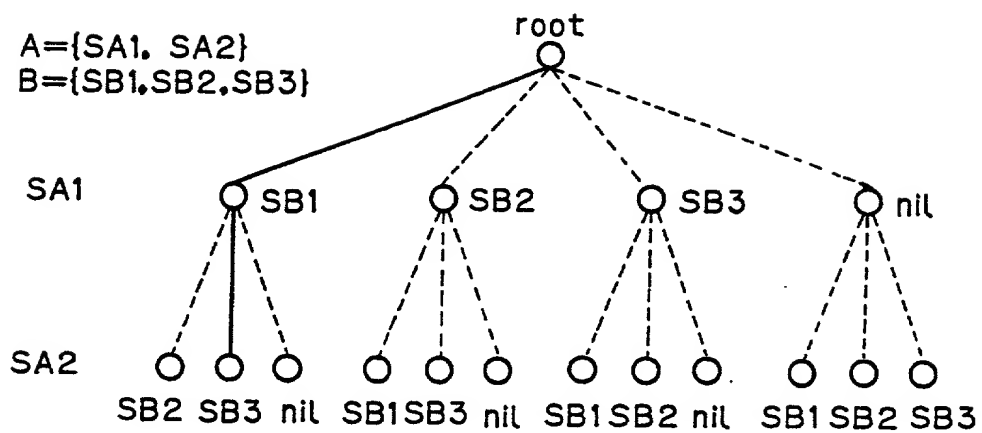
*Fig. 40*

Fig. 41

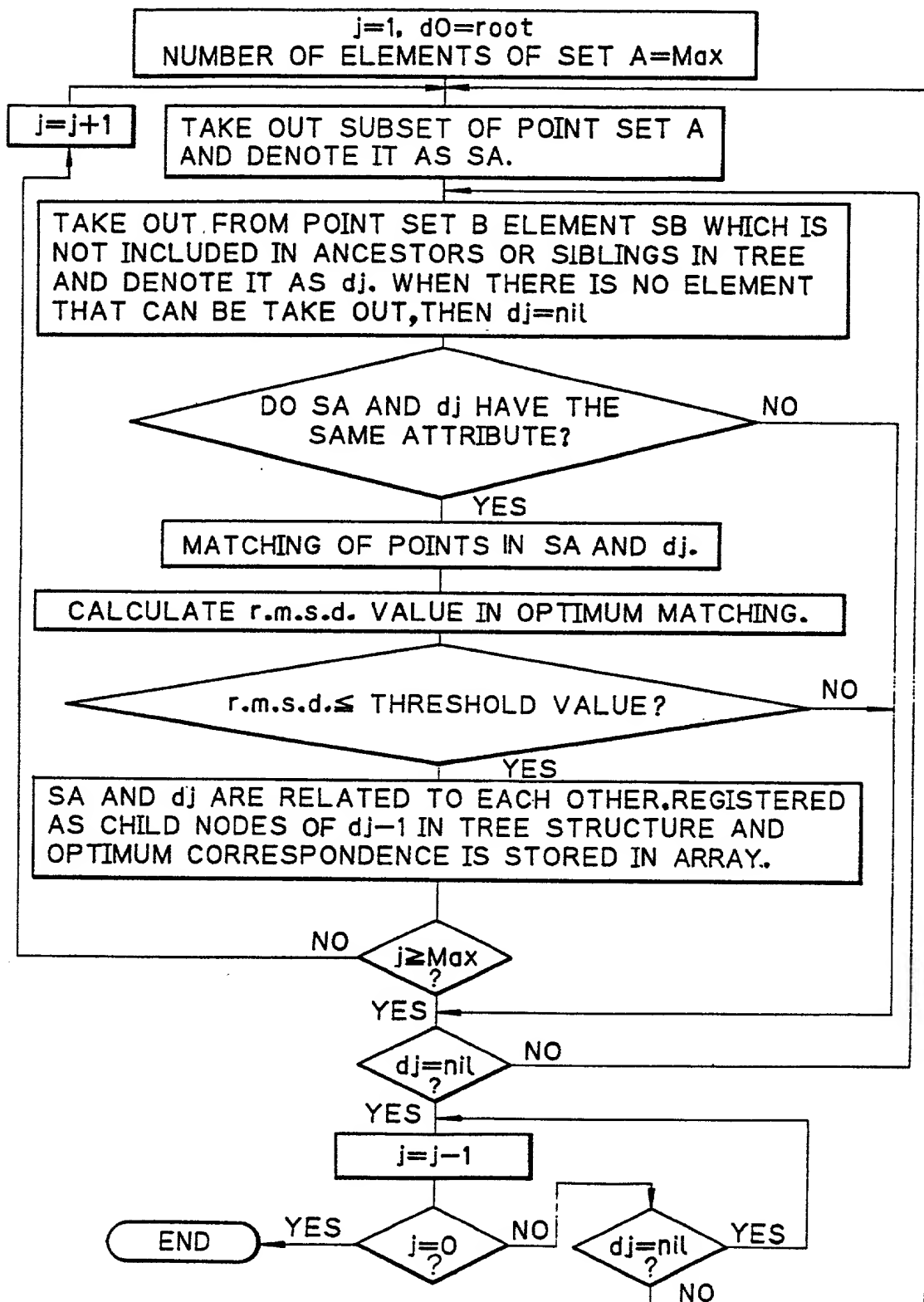


Fig. 42

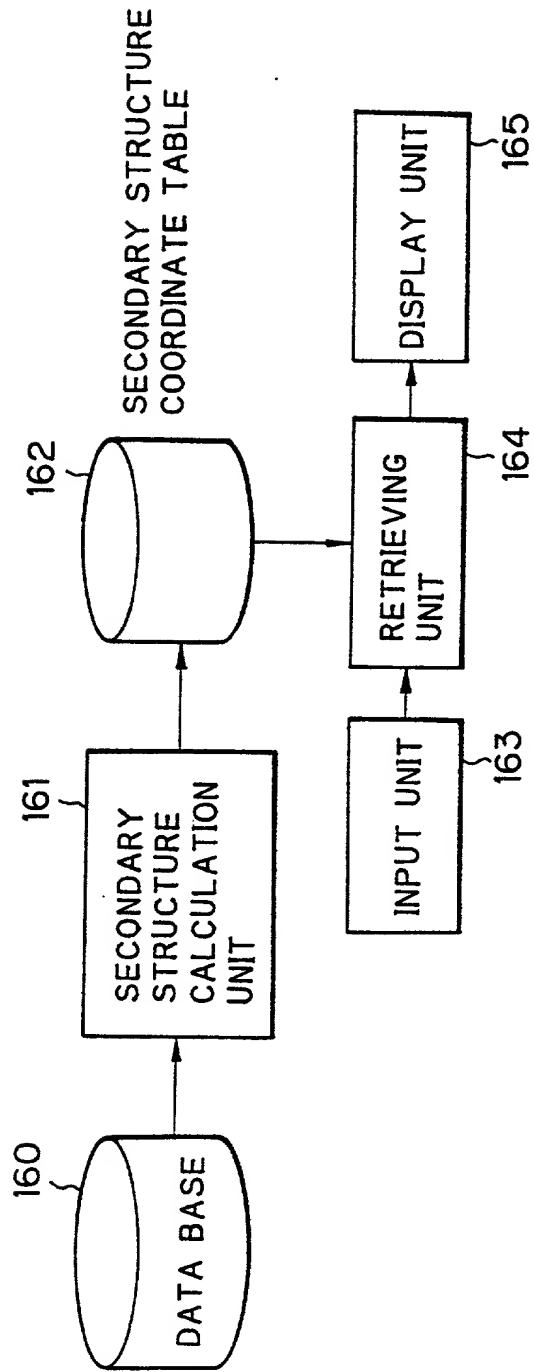
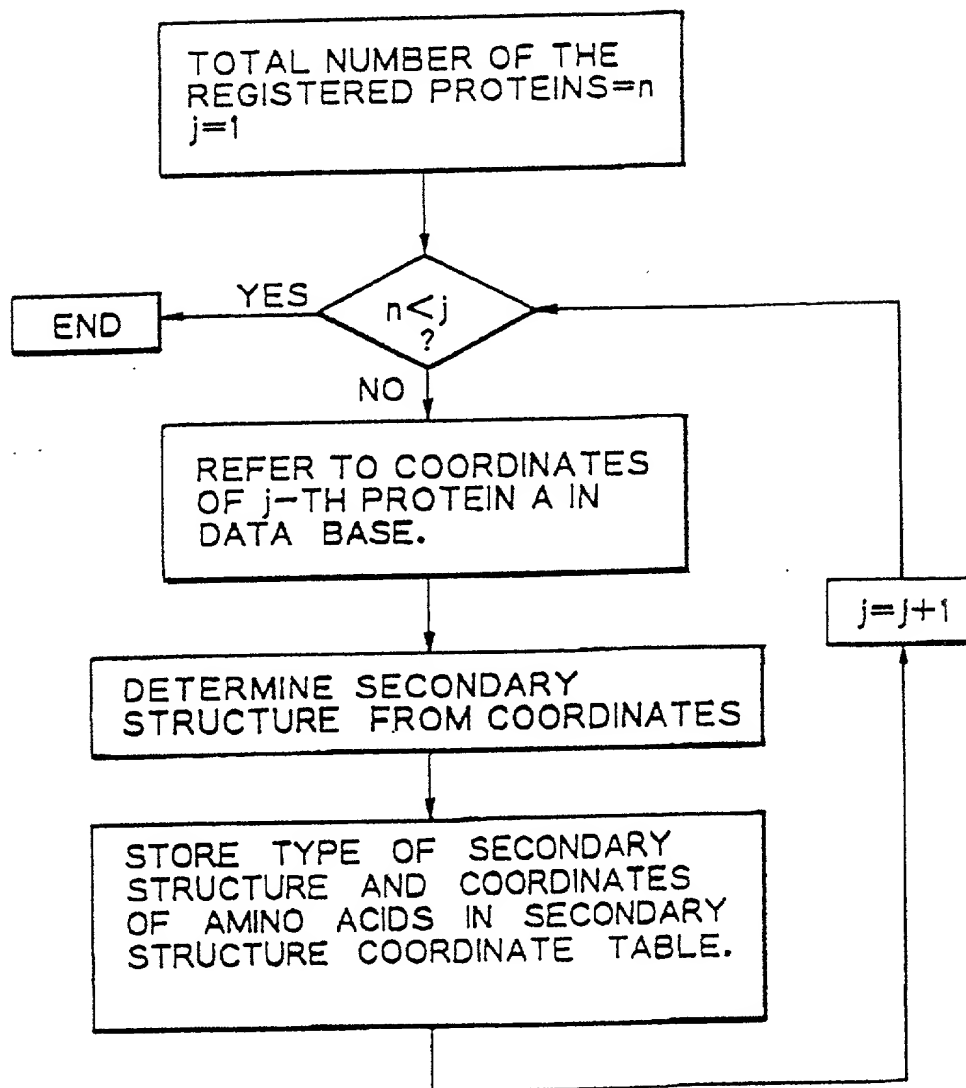




Fig. 43

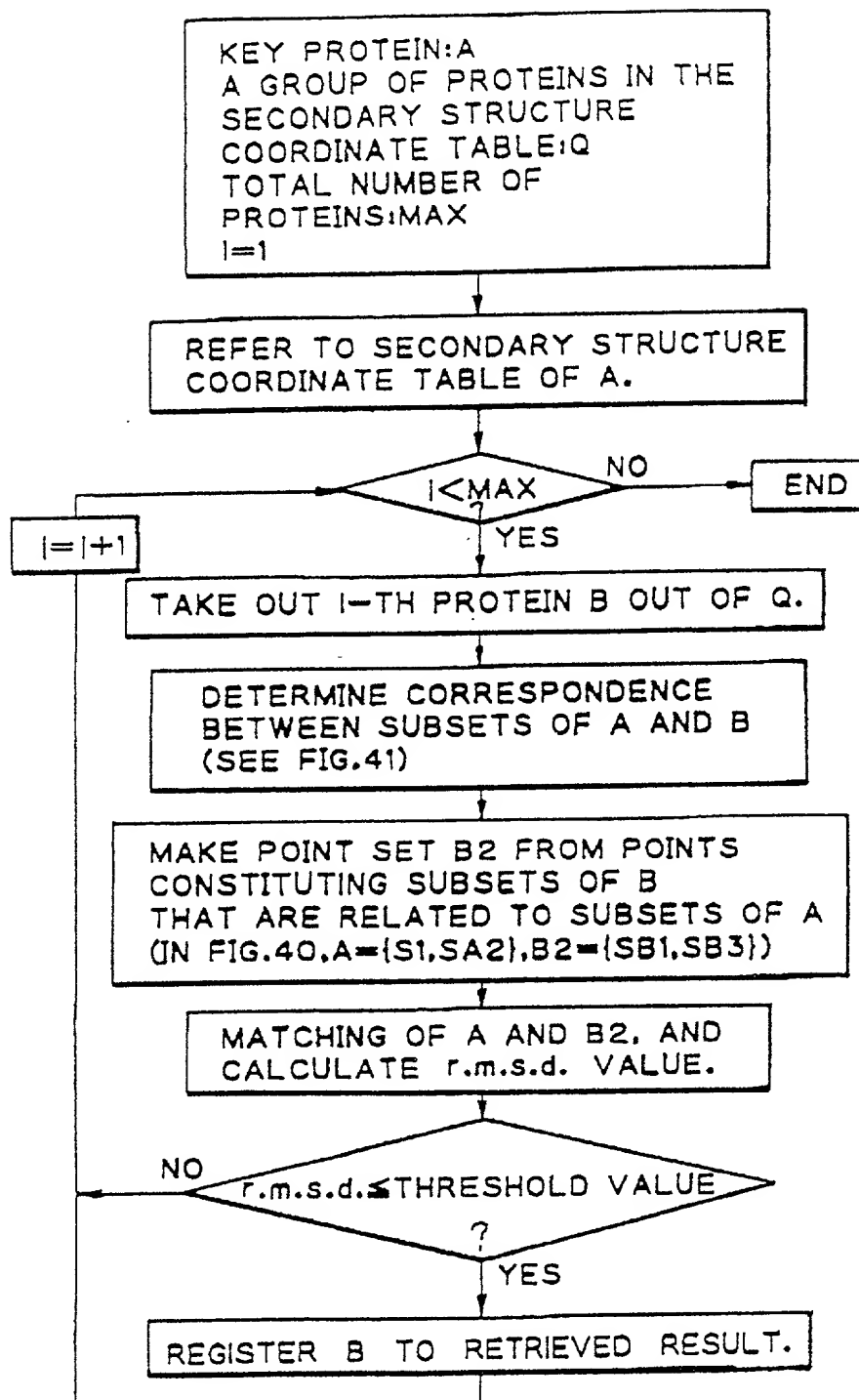


**Fig. 44**

162

SUBSET	COORDINATES	TYPE
S1	$\{X_1, X_2, X_3, X_4, \dots X_a\}$	$\alpha$ - HELIX
S2	$\{X_{a+1}, X_{a+2}, \dots X_b\}$	$\alpha$ - HELIX
S3	$\{X_{b+1}, X_{b+2}, \dots X_c\}$	$\beta$ - SHEET
S4	$\{X_{c+1}, X_{c+2}, \dots X_d\}$	$\beta$ - SHEET
	$\vdots$	$\vdots$
Sn	$\{X_{l+1}, X_{l+2}, \dots X_m\}$	3 - TURN

Fig. 45



**Fig. 46**

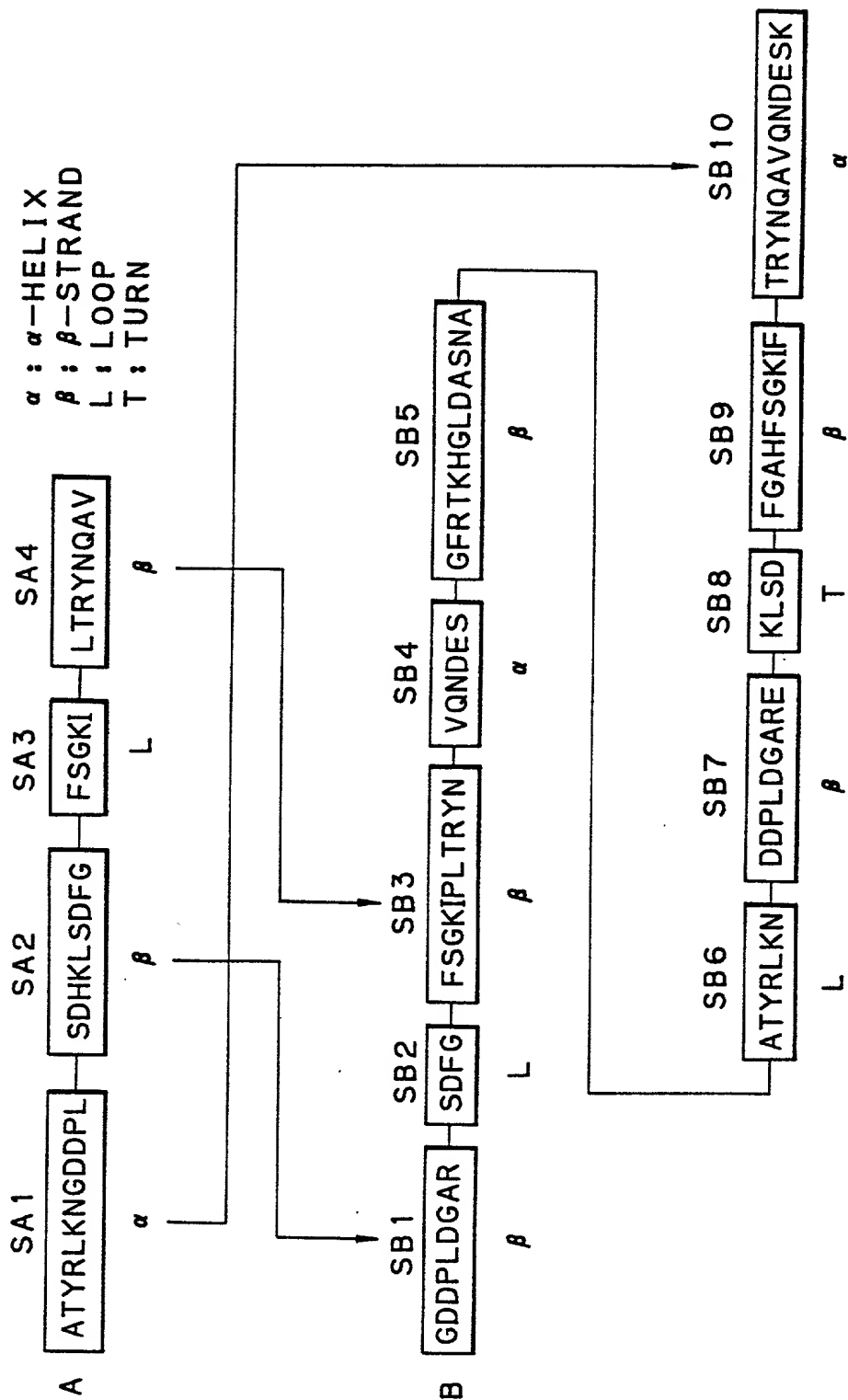
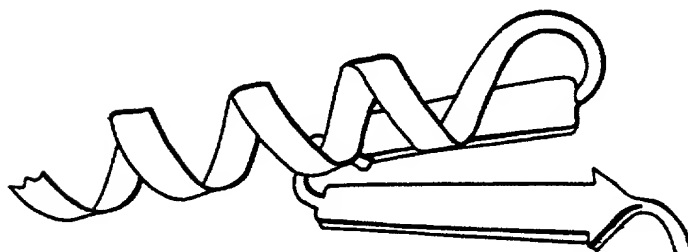
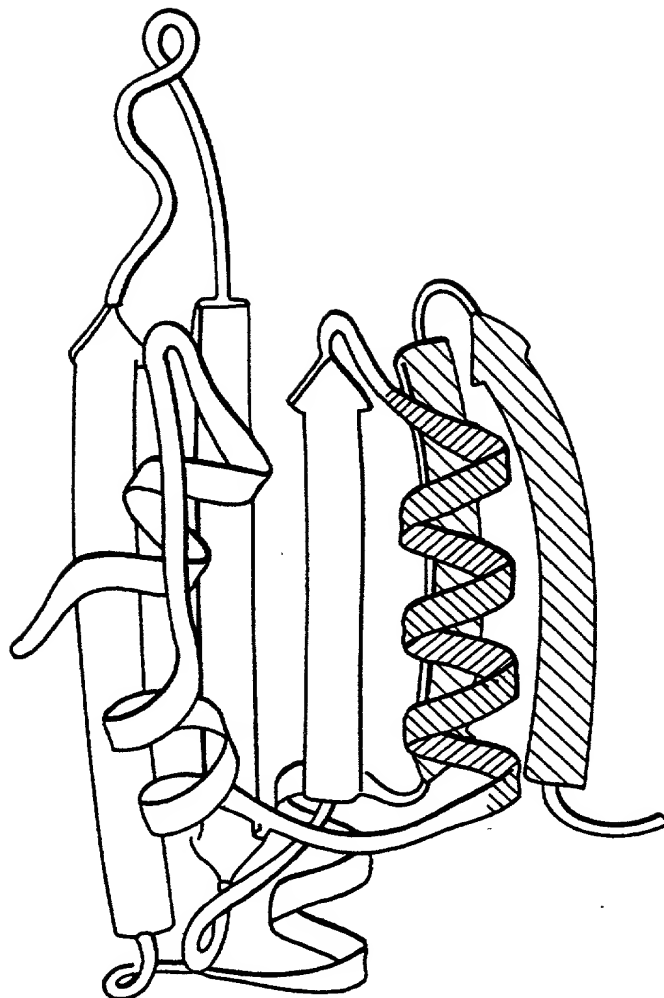


Fig. 47 A



KEY PROTEIN A

Fig. 47 B



PROTEIN B HAVING A SIMILAR STRUCTURE